Integrative Cancer Research Workspace
Pathways Tools Special Interest Group
Mission Statement
DRAFT

The opportunities /needs we address:
The Pathway SIG endeavors to support basic research and ICR tool development by helping to provide the cancer research community with easy access to pathway data and commonly used pathway analysis tools.
- A number of software development challenges are anticipated:
  - Making data and tools easy to use
  - Representing pathway information from high to low level of detail (granularity)
  - Integrating data from existing resources (http://www.cbio.mskcc.org/prl)
- A number of use cases are also anticipated:
  - User wants to find out more information about the context of a favorite gene/protein in a pathway via a web-based database or via programmatic query (for example, webservice)
  - Analyze gene lists from transcriptional profiling and other sources in the context of pathways (e.g. over-representation analysis)
  - Visualization of pathways and of cell state and molecular profile data in the context of pathways
  - User wants to curate their own version of a pathway, based on their own experimental data in addition to publicly-available information.
  - Qualitative pathway modeling
 - Quantitative pathway modeling

What we are doing/will do to address these needs:
The following features have been highlighted as requirements to meet our goals:
  - Common API and object model for pathway information to enable easy integration
  - Common format for pathway information to enable easy sharing
  - Shared curation or review of pathway data
  - Data in a non-redundant format
  - Pathway curation tools
  - More signaling pathway and other cancer relevant data
  - A reliability measure for pathway information

The principles/beliefs that guide our work:
- Cellular and physiological process knowledge is vital for cancer research and pathways define the molecular basis of these processes and provide an organizing scaffold for integrating large amounts of genome-scale information with existing knowledge, which enables biologists to link cohesive subsets of large, unmanageable datasets to concepts they are familiar with
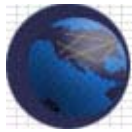
- A working definition of a pathway is a series of molecular interactions and reactions, often forming a network, the start and end points of which is often defined by observation of a detectable phenotype after stimulation or perturbation, such as observing gene expression after stimulating the cell with a peptide growth hormone